

SEQUENCE LISTING

<110> Curtis, Rory A.J., Lora, Jose M. <:120> 46798, A Human Matrix Metalloprotease and Uses Therefore <130> MPI2001-014P1RNM <140> 10/050,216 <141> 2001-01-16 <150> 60/262,252 <151> 2001-01-16 <150> 10 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 2310 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (317)...(1651) <400> 1 gtegacecae gegteeggee gggeeteege ecceteegee tgeettteet teeteeetee 60 eteggteece ggggeegge gaeeegegg eaggeactge eegggetgga egaegtetgg $120\,$ 180 ceggeteceg gegaagggea geggaggage ggeceagage gegeagetag ggeaetggeg aaaccccggg acagtccctc tccgtgcggg ggcggcgcag agcagtccca tccccggggt cocgggegeg getgactgee gg:tggttee etgegegeag tageteeeg ageeggetg caceggagge ggegag atg gte geg ege gte gge ete etg etg ege gee etg Met Val Ala Arg Val Gly Leu Leu Arg Ala Leu 300 cag ctg cta ctg tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga Gln Leu Leu Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly ggc cag gag ctg cgc aag gag gcg gag gca ttc cta gag aag tac gga Gly Gln Glu Leu Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly tac ctc aat gaa cag gtc ccc aaa gct ccc acc tcc act cga ttc agc T_{Σ} r Leu Asn Glu Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser gat gcc atc aga gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc Asp Ala Ile Arg Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly gtg ttg gac cgc gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg Val Leu Asp Arg Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly 592 gtt aca gat acc aac agt tat gcg gcc tgg gct gag agg atc agt gac Val Thr Asp Thr Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp 640 100 ttg ttt gct aga cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca Leu Phe Ala Arg His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala 688 aag caa ggg ggc gcc ctg gcg cac gcc ttc ctg ccc cgc ggc gga gaa Lys Gln Gly Gly Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu 784 geg cae the gae caa gat gag ege tgg tee etg age ege ege ege ggg Ala His Phe Asp Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Gly 150

cgc Arg																832
ctc Leu																880
agg Arg																928
cag Gln 205																976
cca Pro																1024
caa Gln																1072
ttc Phe																1120
GJA aaa																1168
cgt Arg 285																1216
gcg Ala																1264
cga Arg																1312
ctg Leu																1360
ttc Phe																1408
gtg Val 365																1456
ctg Leu																1504
agg Arg																1552
ctc (Leu .																1600
gag Glu																1648
ttc Phe 445	tgaa	ıggca	icc t	ccto	cacct	c ag	jaaac	tggt	ggt	gcto	etca	gggd	caaaa	atc		1701
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His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly 115

Ash Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg 1100

His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly 115

120

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195
Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
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Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile 245

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Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln 275

Glu Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Val Ser Glu Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Asp Ser Glu Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Asp Ser Glu Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Ala Ser Ser Glu Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Ala Asp Ser Glu Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Ala Asp Ser Glu Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Ala Ala Ser Ser Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Ala Ala Asp Ser Ser Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Ala Ala Asp Ser Ser Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Ala Ala Asp Ser Ser Arg Trp Val Gly Leu Pro Pro Asp Ile Glu Ala Ala Ala Ala Ala Asp Ser Ser Arg Trp Val Gly Leu Pro Asp Ile Glu Ala Ala Ala Ala Ala Asp Ser Ser Arg Pro Arg Trp Val Gly Leu Pro Asp Ile Glu Ala Ala Ala Ala Ala Asp Ser Ser Arg Pro Arg Pr Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser 290 295 300 Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg 305 310 315 320 Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala 325 330 335
Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu 340 345 350 Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg 355 360 365 Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp 420 425

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cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga $$ 1 Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg $$ 50 $$ 55 $$ 60	.92												
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cot gaa acg cag ggc cot aaa tac tgc cac tot too tto gat gcc atc 7 Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile 245 250 255	768												
act gta gac agg caa cag caa ctg tac att ttt aaa ggg agc cat ttc Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe 260 265 270	816												
tgg gag gtg gba got gat ggc aac gtc tba gag boo ogt oba otg dag - 8	864												

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Leu Glu Val Met Lys Lys Pro Arg Cys Gly Val Pro Asp Val Gly Glu Glu Ser Asn Thr 50 55 60 50

Phe Arg Thr Phe Pro Gly Ser Pro Lys Trp Ser Lys Asn Asn Leu Leu
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Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp Leu Pro Arg Glu Asp Val
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Asp Asp Ala Ile Arg Arg Ala Phe Gln Val Trp Ser Asp Val Thr Pro
100

Leu Thr Phe Thr Arg Val Ser Asp Gly Glu Ala Asp Ile Met Ile Ser
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The Ala Trp Clu Clu His Clu Arg Phe Tyr Pro Phe Asp Gly Lys Gly Phe Ala Arg Gly Glu His Gly Asp Phe Tyr Pro Phe Asp Gly Lys Gly 130 135 Gly Leu Leu Ala His Ala Phe Ala Pro Gly Pro Gly Ile Gly Ile Gly 145
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Ala Asp Ile Met Ile Ser Phe Gly Ile Lys Glu His Gly Asp Phe Tyr 165 170 175

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Gly His Ser Leu Gly Leu Asp His Ser Lys Asp Pro Gly Ala Leu Met 225 230 235 240
Ser Leu Asp Ala Ile Thr Ser Leu Arg Gly Glu Thr Met Ile Phe Lys
295 300
Asp Arg Phe Phe Trp Arg Leu His Pro Gln Gln Val Asp Ala Glu Leu
305 310 320
Phe Leu Thr Lys Ser Phe Trp Pro Glu Leu Pro Asn Arg Ile Asp Ala 325 330 335

Ala Tyr Glu His Pro Ser His Asp Leu Ile Phe Ile Phe Arg Gly Arg 340 345 350
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Mys Ile Ser Glu Leu Gly Leu Pro Lys Glu Val Lys Lys Ile Ser Ala 370

375

380
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Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro
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385 390 395 400
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450 460 Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe 465 470 475Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala Lys Leu Gln Ala Thr 485

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aac Asn	agt Ser	tat Tyr	gcg Ala 190	gcc Ala	tgg Trp	gct Ala	gag Glu	agg Arg 105	atc Ile	agt Ser	gac Asp	ttg Leu	ttt Phe 110	gct Ala	aga Arg	336
							aag Lys 120									384
aaa Lys	tgg Trp 130	tac Tyr	aag Lys	cag Gln	cac His	ctc Leu 135	tcc Ser	tac Tyr	cgc Arg	ctg Leu	gtg Val 140	aac Asn	tgg Trp	cct Pro	gag Glu	432
cat His 145	ctg Leu	ccg Pro	gag Glu	ccg Pro	gca Ala 150	gtt Val	cgg Arg	ggc Gly	gcc Ala	gtg Val 155	cgc Arg	gcc Ala	gcc Ala	ttc Phe	cag Gln 160	480
ttg Leu	tgg Trp	agc Ser	aac Asn	gtc Val 165	tca Ser	gcg Ala	ctg Leu	gag Glu	ttc Phe 170	tgg Trp	gag Glu	gcc Ala	cca Pro	gcc Ala 175	aca Thr	523
G17 gac	ccc Pro	gct Ala	gac Asp 180	atc Ile	cgg Arg	ctc Leu	acc Thr	ttc Phe 185	ttc Phe	caa Gln	ggg Gly	gac Asp	cac His 190	aac Asn	gat Asp	57 ธ์
Gl ^A aaa	ctg Leu	ggc Gly 195	aat Asn	gcc Ala	ttt Phe	gat Asp	ggc Gly 200	cca Pro	gly ggg	ggc Gly	gcc Ala	ctg Leu 205	gcg Ala	cac His	gcc Ala	624
ttc Phe	ctg Leu 210	ccc Pro	cgc Arg	cgc Arg	ggc Gly	gaa Glu 215	gcg Ala	cac His	ttc Phe	gac Asp	caa Gln 220	gat Asp	gag Glu	cgc Arg	tgg Trp	672
tcc Ser 225	ctg Leu	agc Ser	cgc Arg	cgc Arg	cgc Arg 230	Gly ggg	cgc Arg	aac Asn	ctg Leu	ttc Phe 235	gtg Val	gtg Val	ctg Leu	gcg Ala	cac His 240	720
gag Glu	atc Ile	ggt Gly	cac His	acg Thr 245	ctt Leu	ggc Gly	ctc Leu	acc Thr	cac His 250	tcg Ser	ccc Pro	gcg Ala	ccg Pro	cgc Arg 255	gcg Ala	768
ctc Leu	atg Met	gcg Ala	ccc Pro 260	tac Tyr	tac Tyr	aag Lys	agg Arg	ctg Leu 265	ggc Gly	cgc Arg	gac Asp	gcg Ala	ctg Leu 270	ctc Leu	agc Ser	816
tgg Trp	gac Asp	gac Asp 275	gtg Val	ctg Leu	gcc Ala	gtg Val	cag Gln 280	agc Ser	ctg Leu	tat Tyr	GJA aaa	aag Lys 285	ccc Pro	cta Leu	Gly aaa	864
ggc Gly	tca Ser 290	gtg Val	gcc Ala	gtc Val	cag Gln	ctc Leu 295	cca Pro	gga Gly	aag Lys	ctg Leu	ttc Phe 300	act Thr	gac Asp	ttt Phe	gag Glu	912
acc Thr 305	tgg Trp	gac Asp	tcc Ser	tac Tyr	agc Ser 310	ccc Pro	caa Gln	gga Gly	agg Arg	cgc Arg 315	cct Pro	gaa Glu	acg Thr	cag Gln	ggc Gly 320	960
cct Pro	aaa Lys	tac Tyr	tgc Cys	cac His 325	tct Ser	tcc Ser	ttc Phe	gat Asp	gcc Ala 330	atc Ile	act Thr	gta Val	gac Asp	agg Arg 335	caa Gln	1008
cag Gln	caa Gln	ctg Leu	tac Tyr 340	att Ile	ttt Phe	aaa Lys	Gly ggg	agc Ser 345	cat His	ttc Phe	tgg Trp	gag Glu	gtg Val 350	gca Ala	gct Ala	1056
gat Asp	ggc Gly	aac Asn 355	gtc Val	tca Ser	gag Glu	ccc Pro	cgt Arg 360	cca Pro	ctg Leu	cag Gln	gaa Glu	aga Arg 365	tgg Trp	gtc Val	Gly ggg	1104

	att gag Ile Glu					1152
	aaa ggg Lys Gly 390					1200
	ctc cca Leu Pro 405					1248
	gcc ete Ala Leu					1296
	cgc tac Arg Tyr	l Leu				1344
	ccc cga Pro Arg					1392
	gcc ctg Ala Leu 470					1440
	tac tgg Tyr Trp 485					1488
	tgg gcc Trp Ala					1536
	agc gcc Ser Ala	e *				1563